RAW SEQUENCE LISTING ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: /0/50/,67/

Source: PCT/10

Date Processed by STIC: 7/23/04

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.
PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:
1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY
FOR CRF SUBMISSION AND PATENTIN SOFTWARE QUESTIONS, PLEASE CONTACT
MARK SPENCER, TELEPHONE: 571-272-2510; FAX: 571-273-0221

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE **CHECKER VERSION 4.2 PROGRAM**, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS:
        http://www.uspto.gov/web/offices/pac/checker/chkrnote.htm

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail.
Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom.
Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses:

1. EFS-Bio (**<http://www.uspto.gov/ebc/efs/downloads/documents.htm>** , **EFS Submission User Manual** - ePAVE)
2. U.S. Postal Service: Commissioner for Patents, P.O. Box 1450, Alexandria, VA 22313-1450
3. Hand Carry, Federal Express, United Parcel Service, or other delivery service (EFFECTIVE 06/05/04):
    U.S. Patent and Trademark Office, 220 20th Street S.; Customer Window, Mail Stop Sequence, Crystal Plaza Two, Lobby Room 1B03, Arlington, VA 22202

Revised 05/17/04

Raw Sequence Listing Error Summary

| ERROR DETECTED | SUGGESTED CORRECTION | SERIAL NUMBER: _10/501,671_ |

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

1 _____ Wrapped Nucleics The number/text at the end of each line "wrapped" down to the next line. This may occur if your file
_____ Wrapped Aminos was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will
prevent "wrapping."

2 _____ Invalid Line Length The rules require that a line not exceed 72 characters in length. This includes white spaces.

3 _✓_ Misaligned Amino The numbering under each 5th amino acid is misaligned. Do not use tab codes between numbers;
_____ Numbering use space characters, instead.

4 _____ Non-ASCII The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please
ensure your subsequent submission is saved in ASCII text.

5 _____ Variable Length Sequence(s)_____ contain n's or Xaa's representing more than one residue. **Per Sequence Rules,
each n or Xaa can only represent a single residue.** Please present the maximum number of each
residue having variable length and indicate in the <220>-<223> section that some may be missing.

6 _____ PatentIn 2.0 A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid
_____ "bug" sequences(s) _____. Normally, PatentIn would automatically generate this section from the
previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to
the subsequent amino acid sequence. **This applies to the mandatory <220>-<223> sections for
Artificial or Unknown sequences.**

7 _____ Skipped Sequences Sequence(s) _____ missing. If intentional, please insert the following lines for each skipped sequence:
_____ (OLD RULES) (2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
(i)   SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)
(xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
This sequence is intentionally skipped

Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.

8 _____ Skipped Sequences Sequence(s) _____ missing. If intentional, please insert the following lines for each skipped sequence.
_____ (NEW RULES) <210> sequence id number
<400> sequence id number
000

9 _____ Use of n's or Xaa's Use of n's and/or Xaa's have been detected in the Sequence Listing.
_____ (NEW RULES) Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present.
In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.

10 _____ Invalid <213> Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or
_____ Response scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or
is Artificial Sequence

11 _____ Use of <220> Sequence(s) _____ missing the <220> "Feature" and associated numeric identifiers and responses.
Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or
"Unknown." Please explain source of genetic material in <220> to <223> section.
(See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)

12 _____ PatentIn 2.0 Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file,
_____ "bug" resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence
listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.

13 _____ Misuse of n/Xaa "n" can only represent a single <u>nucleotide</u>; "Xaa" can only represent a single <u>amino acid</u>

RAW SEQUENCE LISTING   DATE: 07/23/2004
PATENT APPLICATION: US/10/501,671   TIME: 15:23:45

         Input Set : A:\PTO.FG.txt
         Output Set: N:\CRF4\07232004\J501671.raw

      3 <110> APPLICANT: Asahi Kasei Kabushiki Kaisha
W--> 4 <120> TITLE OF INVENTION: High-concentration preparation of soluble thrombomodulin
      6 <130> FILE REFERENCE: ASAHI-33
C--> 8 <140> CURRENT APPLICATION NUMBER: US/10/501,671
C--> 8 <141> CURRENT FILING DATE: 2004-07-16
      8 <150> PRIOR APPLICATION NUMBER: JP2002-009951
      9 <151> PRIOR FILING DATE: 2002-01-18
     11 <160> NUMBER OF SEQ ID NOS: 9

_pp 1-6_

Does Not Comply
Corrected Diskette Needed

ERRORED SEQUENCES

     13 <210> SEQ ID NO: 1
     14 <211> LENGTH: 516
     15 <212> TYPE: PRT
     16 <213> ORGANISM: Artificial sequence
     18 <220> FEATURE:
     19 <223> OTHER INFORMATION: Partial amino acid sequence of human-originated soluble
     20   thrombomodulin
     22 <400> SEQUENCE: 1

misaligned amino acid numbers (see item 3 on Error Summary Sheet)

     23 Met Leu Gly Val Leu Val Leu Gly Ala Leu Ala Leu Ala Gly Leu Gly
E--> 24 1   5   5   10   10   15   15
     25 Phe Pro Ala Pro Ala Glu Pro Gln Pro Gly Gly Ser Gln Cys Val Glu
E--> 26   20   20   25   25   30   30
     27 His Asp Cys Phe Ala Leu Tyr Pro Gly Pro Ala Thr Phe Leu Asn Ala
E--> 28   35   40   45
     29 Ser Gln Ile Cys Asp Gly Leu Arg Gly His Leu Met Thr Val Arg Ser
E--> 30   50   55   60
     31 Ser Val Ala Ala Asp Val Ile Ser Leu Leu Leu Asn Gly Asp Gly Gly
E--> 32 65   70   75   80
     33 Val Gly Arg Arg Arg Leu Trp Ile Gly Leu Gln Leu Pro Pro Gly Cys
E--> 34   85   90   95
     35 Gly Asp Pro Lys Arg Leu Gly Pro Leu Arg Gly Phe Gln Trp Val Thr
E--> 36   100   105   110
     37 Gly Asp Asn Asn Thr Ser Tyr Ser Arg Trp Ala Arg Leu Asp Leu Asn
E--> 38   115   120   125
     39 Gly Ala Pro Leu Cys Gly Pro Leu Cys Val Ala Val Ser Ala Ala Glu
E--> 40   130   135   140
     41 Ala Thr Val Pro Ser Glu Pro Ile Trp Glu Glu Gln Gln Cys Glu Val
E--> 42 145   150   155   160
     43 Lys Ala Asp Gly Phe Leu Cys Glu Phe His Phe Pro Ala Thr Cys Arg
E--> 44   165   170   175
     45 Pro Leu Ala Val Glu Pro Gly Ala Ala Ala Ala Ala Val Ser Ile Thr

RAW SEQUENCE LISTING   DATE: 07/23/2004
PATENT APPLICATION: US/10/501,671   TIME: 15:23:45

Input Set : A:\PTO.FG.txt
Output Set: N:\CRF4\07232004\J501671.raw

```
E--> 46            180                   185                        190   same
     47 Tyr Gly Thr Pro Phe Ala Ala Arg Gly Ala Asp Phe Gln Ala Leu Pro        error
E--> 48            195                   200                        205
     49 Val Gly Ser Ser Ala Ala Val Ala Pro Leu Gly Leu Gln Leu Met Cys
E--> 50        210                   215                    220
     51 Thr Ala Pro Pro Gly Ala Val Gln Gly His Trp Ala Arg Glu Ala Pro
E--> 52 225                    230                    235                    240
     53 Gly Ala Trp Asp Cys Ser Val Glu Asn Gly Gly Cys Glu His Ala Cys
E--> 54                245                    250                    255
     55 Asn Ala Ile Pro Gly Ala Pro Arg Cys Gln Cys Pro Ala Gly Ala Ala
E--> 56                260                    265                270
     57 Leu Gln Ala Asp Gly Arg Ser Cys Thr Ala Ser Ala Thr Gln Ser Cys
E--> 58            275                    280                    285
     59 Asn Asp Leu Cys Glu His Phe Cys Val Pro Asn Pro Asp Gln Pro Gly
E--> 60         290                   295                    300
     61 Ser Tyr Ser Cys Met Cys Glu Thr Gly Tyr Arg Leu Ala Ala Asp Gln
E--> 62 305                    310                    315                    320
     63 His Arg Cys Glu Asp Val Asp Asp Cys Ile Leu Glu Pro Ser Pro Cys
E--> 64                325                    330                335
     65 Pro Gln Arg Cys Val Asn Thr Gln Gly Gly Phe Glu Cys His Cys Tyr
E--> 66            340                    345                350
     67 Pro Asn Tyr Asp Leu Val Asp Gly Glu Cys Val Glu Pro Val Asp Pro
E--> 68         355                    360                    365
     69 Cys Phe Arg Ala Asn Cys Glu Tyr Gln Cys Gln Pro Leu Asn Gln Thr
E--> 70     370                    375                380
     71 Ser Tyr Leu Cys Val Cys Ala Glu Gly Phe Ala Pro Ile Pro His Glu
E--> 72 385                    390                    395                    400
     73 Pro His Arg Cys Gln Met Phe Cys Asn Gln Thr Ala Cys Pro Ala Asp
E--> 74                405                    410                    415
     75 Cys Asp Pro Asn Thr Gln Ala Ser Cys Glu Cys Pro Glu Gly Tyr Ile
E--> 76            420                    425                430
     77 Leu Asp Asp Gly Phe Ile Cys Thr Asp Ile Asp Glu Cys Glu Asn Gly
E--> 78         435                    440                    445
     79 Gly Phe Cys Ser Gly Val Cys His Asn Leu Pro Gly Thr Phe Glu Cys
E--> 80     450                    455                    460
     81 Ile Cys Gly Pro Asp Ser Ala Leu Val Arg His Ile Gly Thr Asp Cys
E--> 82 465                    470                    475                    480
     83 Asp Ser Gly Lys Val Asp Gly Gly Asp Ser Gly Ser Gly Glu Pro Pro
E--> 84            485                    490                495
     85 Pro Ser Pro Thr Pro Gly Ser Thr Leu Thr Pro Pro Ala Val Gly Leu
E--> 86            500                    505                    510
     87 Val His Ser Gly
E--> 88            515
     90 <210> SEQ ID NO: 2    1547 (p.3)
     91 <211> LENGTH: (1548) 1547 (p.3)
     92 <212> TYPE: DNA
     93 <213> ORGANISM: Artificial sequence
     95 <220> FEATURE:
     96 <223> OTHER INFORMATION: Partial base sequence of human-originated soluble
```

RAW SEQUENCE LISTING   DATE: 07/23/2004
PATENT APPLICATION: US/10/501,671   TIME: 15:23:45

Input Set : A:\PTO.FG.txt
Output Set: N:\CRF4\07232004\J501671.raw

```
97          thrombomodulin gene
99 <400> SEQUENCE: 2
100 atgcttgggg tcctggtcct tggcgcgctg gccctggccg gcctgggggtt ccccgcaccc    60
101 gcagagccgc agccgggtgg cagccagtgc gtcgagcacg actgcttcgc gctctacccg   120
102 ggccccgcga ccttcctcaa tgccagtcag atctgcgacg gactgcgggg ccacctaatg   180
103 acagtgcgct cctcggtggc tgccgatgtc atttccttgc tactgaacgg cgacggcggc   240
104 gttggccgcc ggcgcctctg gatcggcctg cagctgccac ccggctgcgg cgaccccaag   300
105 cgcctcgggc ccctgcgcgg cttccagtgg gttacgggag acaacaacac cagctatagc   360
106 aggtgggcac ggctcgacct caatggggct cccctctgcg gcccgttgtg cgtcgctgtc   420
107 tccgctgctg aggccactgt gcccagcgag ccgatctggg aggagcagca gtgcgaagtg   480
108 aaggccgatg gcttcctctg cgagttccac ttcccagcca cctgcaggcc actggctgtg   540
109 gagcccggcg ccgcggctgc cgccgtctcg atcacctacg gcaccccgtt cgcggcccgc   600
110 ggagcggact ccaggcgct gccggtgggc agctccgccg cggtggctcc cctcggctta   660
111 cagctaatgt gcaccgcgcc gcccggagcg gtccaggggc actgggccag ggaggcgccg   720
112 ggcgcttggg actgcagcgt ggagaacggc ggctgcgagc acgcgtgcaa tgcgatccct   780
113 ggggctcccc gctgccagtg cccagccggc gccgccctgc aggcagacgg gcgctcctgc   840
114 accgcatccg cgacgcagtc ctgcaacgac ctctgcgagc acttctgcgt cccaacccc   900
115 gaccagccgg gctcctactc gtgcatgtgc gagaccggct accggctggc ggccgaccaa   960
116 caccggtgcg aggacgtgga tgactgcata ctggagccca gtccgtgtcc gcagcgctgt  1020
117 gtcaacacac agggtggctt cgagtgccac tgctaccta actacgacct ggtggacggc  1080
118 gagtgtgtgg agcccgtgga cccgtgcttc agagccaact gcgagtacca gtgccagccc  1140
119 ctgaaccaaa ctagctacct ctgcgtctgc gccgagggct cgcgcccat tccccacgag  1200
120 ccgcacaggt gccagatgtt ttgcaaccag actgcctgtc cagccgactg cgaccccaac  1260
121 acccaggcta gctgtgagtg ccctgaaggc tacatcctgg acgacggttt catctgcacg  1320
122 gacatcgacg agtgcgaaaa cggcggcttc tgctccgggg tgtgccacaa cctccccggt  1380
```

E--> 123 accttcgagt gcatctgcgg gcccgactcg gcccttgtcc gccacattgg caccgac(T)(1440)1439

E--> 124 gactccggca aggtggacgg tggcgacagc ggctctggcg agcccccgcc cagcccgacg (1500)1499

E--> 125 cccggctcca ccttgactcc tccggccgtg gggctcgtgc attcgggc   1547 (1548)

[handwritten annotations in right margin: "FYI: periods are invalid nucleic acid designator"]

[handwritten annotation: "This is a group of 9 positions, not 10."]

```
127 <210> SEQ ID NO: 3
128 <211> LENGTH: 132
129 <212> TYPE: PRT
130 <213> ORGANISM: Artificial sequence
132 <220> FEATURE:
133 <223> OTHER INFORMATION: Partial amino acid sequence of human-originated soluble
134        thrombomodulin
```

E--> 136 <400> SEQUENCE: (8)3 *[handwritten: ←change to]*

```
137 Met Leu Gly Val Leu Val Leu Gly Ala Leu Ala Leu Ala Gly Leu Gly
```

E--> 138 1   5   10   15

```
139 Phe Pro Asp Pro Cys Phe Arg Ala Asn Cys Glu Tyr Gln Cys Gln Pro
```

E--> 140   20   25   30

```
141 Leu Asn Gln Thr Ser Tyr Leu Cys Val Cys Ala Glu Gly Phe Ala Pro
```

E--> 142   35   40   45

```
143 Ile Pro His Glu Pro His Arg Cys Gln Met Phe Cys Asn Gln Thr Ala
```

E--> 144   50   55   60

```
145 Cys Pro Ala Asp Cys Asp Pro Asn Thr Gln Ala Ser Cys Glu Cys Pro
```

E--> 146 65   70   75   80

```
147 Glu Gly Tyr Ile Leu Asp Asp Gly Phe Ile Cys Thr Asp Ile Asp Glu
```

E--> 148   85   90   95

```
149 Cys Glu Asn Gly Gly Phe Cys Ser Gly Val Cys His Asn Leu Pro Gly
```

[handwritten annotation: "misaligned amino acid numbers"]

[handwritten annotation: "see p. 4"]

misaligned numbers

```
E--> 150              100                    105                    110
     151 Thr Phe Glu Cys Ile Cys Gly Pro Asp Ser Ala Leu Val Arg His Ile
E--> 152              115                    120                    125
     153 Gly Thr Asp Cys
E--> 154      130
     174 <210> SEQ ID NO: 5
     175 <211> LENGTH: 516
     176 <212> TYPE: PRT
     177 <213> ORGANISM: Artificial sequence
     179 <220> FEATURE:
     180 <223> OTHER INFORMATION: Partial amino acid sequence of human-originated soluble
     181       thrombomodulin
     183 <400> SEQUENCE: 5
     184 Met Leu Gly Val Leu Val Leu Gly Ala Leu Ala Leu Ala Gly Leu Gly
E--> 185   1        •        5                    10                   15
     186 Phe Pro Ala Pro Ala Glu Pro Gln Pro Gly Gly Ser Gln Cys Val Glu
E--> 187              20                    25                    30
     188 His Asp Cys Phe Ala Leu Tyr Pro Gly Pro Ala Thr Phe Leu Asn Ala
E--> 189           35                    40                    45
     190 Ser Gln Ile Cys Asp Gly Leu Arg Gly His Leu Met Thr Val Arg Ser
E--> 191           50                    55                    60
     192 Ser Val Ala Ala Asp Val Ile Ser Leu Leu Leu Asn Gly Asp Gly Gly
E--> 193   65                    70                    75                    80
     194 Val Gly Arg Arg Arg Leu Trp Ile Gly Leu Gln Leu Pro Pro Gly Cys
E--> 195              85                    90                    95
     196 Gly Asp Pro Lys Arg Leu Gly Pro Leu Arg Gly Phe Gln Trp Val Thr
E--> 197              100                    105                    110
     198 Gly Asp Asn Asn Thr Ser Tyr Ser Arg Trp Ala Arg Leu Asp Leu Asn
E--> 199           115                    120                    125
     200 Gly Ala Pro Leu Cys Gly Pro Leu Cys Val Ala Val Ser Ala Ala Glu
E--> 201           130                    135                    140
     202 Ala Thr Val Pro Ser Glu Pro Ile Trp Glu Glu Gln Gln Cys Glu Val
E--> 203   145                    150                    155                    160
     204 Lys Ala Asp Gly Phe Leu Cys Glu Phe His Phe Pro Ala Thr Cys Arg
E--> 205              165                    170                    175
     206 Pro Leu Ala Val Glu Pro Gly Ala Ala Ala Ala Ala Val Ser Ile Thr
E--> 207              180                    185                    190
     208 Tyr Gly Thr Pro Phe Ala Ala Arg Gly Ala Asp Phe Gln Ala Leu Pro
E--> 209              195                    200                    205
     210 Val Gly Ser Ser Ala Ala Val Ala Pro Leu Gly Leu Gln Leu Met Cys
E--> 211           210                    215                    220
     212 Thr Ala Pro Pro Gly Ala Val Gln Gly His Trp Ala Arg Glu Ala Pro
E--> 213   225                    230                    235                    240
     214 Gly Ala Trp Asp Cys Ser Val Glu Asn Gly Gly Cys Glu His Ala Cys
E--> 215              245                    250                    255
     216 Asn Ala Ile Pro Gly Ala Pro Arg Cys Gln Cys Pro Ala Gly Ala Ala
E--> 217           260                    265                    270
     218 Leu Gln Ala Asp Gly Arg Ser Cys Thr Ala Ser Ala Thr Gln Ser Cys
E--> 219           275                    280                    285
```

misaligned amino acid numbers

p.5

RAW SEQUENCE LISTING
PATENT APPLICATION: US/10/501,671

DATE: 07/23/2004
TIME: 15:23:45

Input Set : A:\PTO.FG.txt
Output Set: N:\CRF4\07232004\J501671.raw

```
      220 Asn Asp Leu Cys Glu His Phe Cys Val Pro Asn Pro Asp Gln Pro Gly      same
E--> 221       290                   295                   300                 env
      222 Ser Tyr Ser Cys Met Cys Glu Thr Gly Tyr Arg Leu Ala Ala Asp Gln
E--> 223 305                   310                   315                       320
      224 His Arg Cys Glu Asp Val Asp Asp Cys Ile Leu Glu Pro Ser Pro Cys
E--> 225                   325                   330                       335
      226 Pro Gln Arg Cys Val Asn Thr Gln Gly Gly Phe Glu Cys His Cys Tyr
E--> 227                   340                   345               350
      228 Pro Asn Tyr Asp Leu Val Asp Gly Glu Cys Val Glu Pro Val Asp Pro
E--> 229           355                   360                   365
      230 Cys Phe Arg Ala Asn Cys Glu Tyr Gln Cys Gln Pro Leu Asn Gln Thr
E--> 231       370                   375                   380
      232 Ser Tyr Leu Cys Val Cys Ala Glu Gly Phe Ala Pro Ile Pro His Glu
E--> 233 385                   390                   395                       400
      234 Pro His Arg Cys Gln Met Phe Cys Asn Gln Thr Ala Cys Pro Ala Asp
E--> 235                   405                   410                       415
      236 Cys Asp Pro Asn Thr Gln Ala Ser Cys Glu Cys Pro Glu Gly Tyr Ile
E--> 237                   420                   425               430
      238 Leu Asp Asp Gly Phe Ile Cys Thr Asp Ile Asp Glu Cys Glu Asn Gly
E--> 239           435                   440                   445
      240 Gly Phe Cys Ser Gly Val Cys His Asn Leu Pro Gly Thr Phe Glu Cys
E--> 241       450                   455                   460
      242 Ile Cys Gly Pro Asp Ser Ala Leu Ala Arg His Ile Gly Thr Asp Cys
E--> 243 465                   470                   475                       480
      244 Asp Ser Gly Lys Val Asp Gly Gly Asp Ser Gly Ser Gly Glu Pro Pro
E--> 245                   485                   490                   495
      246 Pro Ser Pro Thr Pro Gly Ser Thr Leu Thr Pro Pro Ala Val Gly Leu
E--> 247                   500                   505                   510
      248 Val His Ser Gly
E--> 249               515
      288 <210> SEQ ID NO: 7
      289 <211> LENGTH: 132
      290 <212> TYPE: PRT
      291 <213> ORGANISM: Artificial sequence
W--> 292 <220> FEATURE:
      293 <223> OTHER INFORMATION: Partial amino acid sequence of human-originated soluble
      294        thrombomodulin
      296 <400> SEQUENCE: 7
      297 Met Leu Gly Val Leu Val Leu Gly Ala Leu Ala Leu Ala Gly Leu Gly
E--> 298   1                   5                   10                      15
      299 Phe Pro Asp Pro Cys Phe Arg Ala Asn Cys Glu Tyr Gln Cys Gln Pro
E--> 300               20                   25                      30
      301 Leu Asn Gln Thr Ser Tyr Leu Cys Val Cys Ala Glu Gly Phe Ala Pro
E--> 302           35                   40                      45
      303 Ile Pro His Glu Pro His Arg Cys Gln Met Phe Cys Asn Gln Thr Ala
E--> 304       50                   55                   60
      305 Cys Pro Ala Asp Cys Asp Pro Asn Thr Gln Ala Ser Cys Glu Cys Pro
E--> 306 65                   70                   75                          80
      307 Glu Gly Tyr Ile Leu Asp Asp Gly Phe Ile Cys Thr Asp Ile Asp Glu
```

Misaligned amino acid numbers

P. 6

RAW SEQUENCE LISTING   DATE: 07/23/2004
PATENT APPLICATION: **US/10/501,671**   TIME: 15:23:45

Input Set : **A:\PTO.FG.txt**
Output Set: **N:\CRF4\07232004\J501671.raw**

misaligned amino acid numbers

```
E--> 308                    85                    90                              95
     309 Cys Glu Asn Gly Gly Phe Cys Ser Gly Val Cys His Asn Leu Pro Gly
E--> 310                   100                   105                       110
     311 Thr Phe Glu Cys Ile Cys Gly Pro Asp Ser Ala Leu Ala Arg His Ile
E--> 312          115                   120                    125
     313 Gly Thr Asp Cys
E--> 314        130
     334 <210> SEQ ID NO: 9
     335 <211> LENGTH: 21
     336 <212> TYPE: DNA
     337 <213> ORGANISM: Artificial sequence
     339 <220> FEATURE:
     340 <223> OTHER INFORMATION: Synthetic DNA for mutation
     342 <400> SEQUENCE: 9
     343 aatgtggcgg gcaagggccg a                                          21
E--> 349 (1/12) delete
```

RAW SEQUENCE LISTING ERROR SUMMARY   DATE: 07/23/2004
PATENT APPLICATION: **US/10/501,671**   TIME: 15:23:46

Input Set : **A:\PTO.FG.txt**
Output Set: **N:\CRF4\07232004\J501671.raw**

Invalid Line Length:
The rules require that a line not exceed 72 characters in length. This includes spaces.

Seq#:1; Line(s) 32
Seq#:3; Line(s) 146
Seq#:4; Line(s) 172
Seq#:7; Line(s) 306
Seq#:8; Line(s) 332

VERIFICATION SUMMARY
PATENT APPLICATION: **US/10/501,671**

DATE: 07/23/2004
TIME: 15:23:46

Input Set : **A:\PTO.FG.txt**
Output Set: **N:\CRF4\07232004\J501671.raw**

L:4 M:283 W: Missing Blank Line separator, <120> field identifier
L:8 M:270 C: Current Application Number differs, Replaced Current Application No
L:8 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:24 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:1
M:332 Repeated in SeqNo=1
L:123 M:254 E: No. of Bases conflict, LENGTH:Input:1440 Counted:1439 SEQ:2
L:123 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:1
M:254 Repeated in SeqNo=2
L:125 M:252 E: No. of Seq. differs, <211> LENGTH:Input:1548 Found:1547 SEQ:2
L:136 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQUENCE ID NOS:3 differs:8
L:138 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:8
M:332 Repeated in SeqNo=3
L:185 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:5
M:332 Repeated in SeqNo=5
L:292 M:283 W: Missing Blank Line separator, <220> field identifier
L:298 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:7
M:332 Repeated in SeqNo=7
L:349 M:254 E: No. of Bases conflict, LENGTH:Input:12 Counted:22 SEQ:9
L:349 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:2
L:349 M:252 E: No. of Seq. differs, <211> LENGTH:Input:21 Found:22 SEQ:9